

Input Set: I339352.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

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1 <110> APPLICANT: REED-GITOMER, BERENICE Y.
2   PAK, CHARLES Y.C.
3 <120> TITLE OF INVENTION: ABSORPTIVE HYPERCALCIURIA LOCUS ON HUMAN CHROMOSOME 1
4 <130> FILE REFERENCE: UTSD:553
5 <140> CURRENT APPLICATION NUMBER: US/09/339,352
6 <141> CURRENT FILING DATE: 1999-06-23
7 <160> NUMBER OF SEQ ID NOS: 6
8 <170> SOFTWARE: PatentIn Ver. 2.0
9 <210> SEQ ID NO 1
10 <211> LENGTH: 2567
11 <212> TYPE: DNA
12 <213> ORGANISM: Human
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16   gtcacctcca acgtcattaa aagaaatctc tctgatccag ctggatagca tgagactttc 180
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21   ggatcacggt gaagaggaac agcttcgtga actggagaat gaggtgatcg agtgccacag 480
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24   ccactgcccga ggcagggact tcattcccta tcacacttcc acagtgaata ttcggctcaa 660
25   cgcttttagac atggatgcca ttaaaaagat ggctatgtct catggattta aaagatgcat 720
26   gagactggga gatactgcct caccttatta tattcttcaa gtctgatctt accttggtgt 780
27   gcacacgtgc taagatttgc ctaatgatgt tgggagggtga agctgaagtg atgagagttg 840
28   tgcagggact tacttctcca tccacctccc aaaatgaccc tggcaaagga agtgggggtg 900
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47 agacccaggt atgccagact tcaggaatgg gacaactttt acaaattttc caatagagct 2040
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58 &lt;211&gt; LENGTH: 372

59 &lt;212&gt; TYPE: PRT

60 &lt;213&gt; ORGANISM: Human

61 &lt;400&gt; SEQUENCE: 2

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65 20 25 30
66 Thr Phe Tyr Ser Leu Lys Gly Glu Val Cys Phe Asn Met Gly Gln Ile
67 35 40 45
68 Val Leu Ala Lys Lys Met Leu Arg Lys Ala Leu Lys Leu Leu Asn Arg
69 50 55 60
70 Ile Phe Pro Tyr Asn Leu Ile Ser Leu Phe Leu His Ile His Val Glu
71 65 70 75 80
72 Lys Asn Arg His Phe His Tyr Val Asn Arg Gln Ala Gln Glu Ser Pro
73 85 90 95
74 Pro Pro Gly Lys Lys Arg Leu Ala Gln Leu Tyr Arg Gln Thr Val Cys
75 100 105 110
76 Leu Ser Leu Leu Trp Arg Ile Tyr Ser Tyr Ser Tyr Leu Phe His Cys
77 115 120 125
78 Lys Tyr Tyr Ala His Leu Ala Val Met Met Gln Met Asn Thr Ala Leu
79 130 135 140
80 Glu Thr Gln Asn Cys Phe Gln Ile Ile Lys Ala Tyr Leu Asp Tyr Ser
81 145 150 155 160
82 Leu Tyr His His Leu Ala Gly Tyr Lys Gly Val Trp Phe Lys Tyr Glu
83 165 170 175
84 Val Met Ala Met Glu His Ile Phe Asn Leu Pro Leu Lys Gly Glu Gly
85 180 185 190
86 Ile Glu Ile Val Ala Tyr Val Ala Glu Thr Leu Val Phe Asn Lys Leu
87 195 200 205
88 Ile Met Gly His Leu Asp Leu Ala Ile Glu Leu Gly Ser Arg Ala Leu
89 210 215 220
90 Gln Met Trp Ala Leu Leu Gln Asn Pro Asn Arg His Tyr Gln Ser Leu
91 225 230 235 240
92 Cys Arg Leu Ser Arg Cys Leu Leu Leu Asn Ser Arg Tyr Pro Gln Leu
93 245 250 255
94 Ile Gln Val Leu Gly Arg Leu Trp Glu Leu Ser Val Thr Gln Glu His
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96      Ile Phe Ser Lys Ala Phe Phe Tyr Phe Val Cys Leu Asp Ile Leu Leu
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98      Tyr Ser Gly Phe Val Tyr Arg Thr Phe Glu Glu Cys Leu Glu Phe Ile
99          290          295          300
100     His Gln Tyr Glu Asn Asn Arg Ile Leu Lys Phe His Ser Gly Leu Leu
101     305          310          315          320
102     Leu Gly Leu Tyr Ser Ser Val Ala Ile Trp Glu Cys Glu Ala Gly Val
103          325          330          335
104     Gly Arg Arg Leu His Thr Ser Arg Asp Pro Gly Met Pro Asp Phe Arg
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145           tgattaggag cacagcctca gtgc

24

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Line ? Error/Warning

Original Text

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